

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: PERSSON, MATS AXEL
ALLANDER, TOBIAS ERIK
- (ii) TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
HEPATITIS C VIRUS (HCV) E2 ANTIGEN
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: ROBINS & ASSOCIATES
 - (B) STREET: 90 MIDDLEFIELD ROAD, SUITE 200
 - (C) CITY: MENLO PARK
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94025
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/844,215
 - (B) FILING DATE: 17-APR-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/635,109
 - (B) FILING DATE: 19-APR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MCCracken, THOMAS P.
 - (B) REGISTRATION NUMBER: 38,548
 - (C) REFERENCE/DOCKET NUMBER: 80146.002
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650) 325-7812
 - (B) TELEFAX: (650) 325-7823

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Val	Arg	Lys	Pro	Gly
1				5					10					15	

Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Gly
			20					25					30		
His	Val	Ile	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp
		35					40					45			
Met	Gly	Glu	Ser	Ile	Pro	Ile	Phe	Gly	Ser	Ala	Asn	Tyr	Ala	Gln	Asn
	50					55					60				
Tyr	Ala	Gln	Lys	Phe	Arg	Asp	Arg	Val	Ser	Ile	Ile	Ala	Asp	Glu	Ser
65					70					75				80	
Thr	Ser	Thr	Ser	Phe	Ile	Glu	Leu	Ser	Asn	Leu	Arg	Ser	Asp	Asp	Thr
				85					90					95	
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Pro	Pro	Arg	Tyr	Cys	Ser	Ala	Gly
			100					105					110		
Arg	Cys	Tyr	Pro	Gly	Phe	Phe	Gln	Gln	Trp	Gly	Gln	Gly	Thr	Leu	Val
		115					120					125			
Thr	Val	Ser	Ser												
			130												

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly
1				5					10					15	
Ser	Ser	Val	Lys	Val	Ser	Cys	Gln	Val	Phe	Gly	Asp	Thr	Phe	Ser	Arg
			20					25					30		
Tyr	Thr	Ile	Gln	Trp	Leu	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Pro	Glu	Trp
		35					40					45			
Met	Gly	Asn	Ile	Ile	Pro	Val	Tyr	Asn	Thr	Pro	Asn	Tyr	Ala	Gln	Lys
	50					55					60				
Phe	Gln	Gly	Arg	Leu	Ser	Ile	Thr	Ala	Asp	Asp	Ser	Thr	Ser	Thr	Ala
65					70				75					80	
Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe
				85					90					95	
Cys	Ala	Arg	Val	Val	Ile	Pro	Asn	Ala	Ile	Arg	His	Thr	Met	Gly	Tyr
			100					105					110		
Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	
1				5					10					15		
Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Gly	
			20					25					30			
His	Val	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	
		35					40					45				
Met	Gly	Gly	Ser	Ile	Ser	Phe	Phe	Gly	Thr	Ser	Asn	Ser	Ala	Gln	Lys	
	50					55					60					
Phe	Gln	Gly	Arg	Val	Ser	Ile	Thr	Ala	Asp	Glu	Ser	Ala	Ser	Thr	Ala	
65					70				75						80	
Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Ile	Tyr	Tyr	
				85					90					95		
Cys	Ala	Lys	Asp	Pro	Pro	Arg	Phe	Cys	Ser	Gly	Gly	Asn	Cys	Tyr	Pro	
			100					105					110			
Gly	Phe	Phe	Gln	Gln	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	
		115					120					125				

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Lys	Thr	Tyr	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				

Ala	Gly	Ile	Ser	Phe	Asp	Gly	Ser	Asn	Gln	Tyr	Tyr	Ala	Asp	Ser	Val
50						55					60				
Lys	Gly	Arg	Phe	Ile	Val	Ser	Arg	Asp	Asn	Ser	Arg	Asp	Thr	Val	Phe
65					70					75					80
Leu	Gln	Met	Ser	Ser	Leu	Arg	Leu	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Thr	Glu	Gly	Ser	Pro	Phe	Gly	Ser	Ile	Lys	Gly	Arg	Tyr	Tyr	Leu
			100					105					110		
Glu	Asn	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ala	Tyr
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35				40						45			
Ala	Gly	Ile	Trp	Phe	Asp	Gly	Ser	Asn	Gln	Tyr	Tyr	Ser	Asp	Ser	Val
		50				55					60				
Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Arg	Asn	Thr	Leu	Phe
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Thr	Glu	Val	Leu	Phe	Gly	Ser	Ile	Lys	Gly	Arg	Tyr	Tyr	Leu	Glu
			100					105					110		
Asn	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
		115					120								

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gly	
1			5				10						15			
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Arg	Ser	Ser	
			20				25						30			
His	Trp	Trp	Ser	Trp	Val	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
			35				40					45				
Ile	Gly	Glu	Val	Phe	Phe	Ser	Gly	Ser	Thr	Ile	Tyr	Asn	Pro	Ser	Leu	
	50					55					60					
Asn	Asp	Arg	Val	Phe	Met	Ser	Val	Asp	Lys	Ser	Lys	Asp	Gln	Val	Ser	
65					70					75					80	
Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Arg	Ser	Pro	Ile	Lys	Met	Asn	Gln	Gly	Arg	Met	Met	Leu	Asp	Ala	
			100					105					110			
Phe	Asp	Ile	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ile	Val	Ser	Ser			
		115					120					125				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Ser	Glu	Val	Lys	Lys	Pro	Gly	Ser	
1			5				10						15			
Ser	Val	Lys	Val	Ser	Cys	Arg	Ala	Ser	Gly	Gly	Ser	Phe	Arg	Ser	Tyr	
			20				25						30			
Asn	Phe	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35				40						45				
Gly	Gly	Ile	Ile	Pro	Met	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	
	50					55					60					
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ala	Thr	Gly	Tyr	
65				70						75					80	

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Met	Pro	Tyr	Pro	Lys	His	Cys	Ser	Arg	Gly	Ser	Cys	Trp	Gly	Trp
			100					105					110		
Phe	Asp	Pro	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu
1				5				10					15		
Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Asn	Tyr
			20				25					30			
Leu	Ala	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35				40					45				
Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
	50				55					60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro
	65			70				75						80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Leu	Tyr	Gly	Asn	Ser	Arg	Trp
			85					90					95		
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu
1				5					10					15	
Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Asn	Lys	Tyr	Leu
			20					25					30		
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
		35					40					45			
Asp	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser
		50				55					60				
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Pro	Glu
65					70					75				80	
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Arg	Ser	Asp	Trp	Val	Thr	Phe
				85					90					95	
Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys							
			100					105							

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu
1				5					10					15	
Arg	Ala	Thr	Leu	Ser	Cys	Gly	Ala	Ser	Gln	Ser	Val	Arg	Ser	Asn	Tyr
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
		35					40					45			
Tyr	Gly	Val	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
		50				55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro
65					70					75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro	Arg
				85					90					95	
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys					
			100					105							

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly	Glu
1				5					10					15	
Arg	Ala	Ser	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Gly	Asn	Asn	Leu
			20					25					30		
Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr
		35					40					45			
Gly	Gly	Asn	Thr	Arg	Ala	Thr	Gly	Thr	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu
65				70					75					80	
Asp	Phe	Ala	Val	Tyr	Phe	Cys	Gln	His	Tyr	Ser	Thr	Trp	Pro	Leu	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Phe	Lys						
			100						105						

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala	Glu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Val	Gly	Glu
1				5					10					15	
Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Tyr	Ser	Gly	Tyr
			20					25					30		
Leu	Gly	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Arg	Leu	Leu	Ile
		35					40					45			
Tyr	Gly	Ala	Ser	Asn	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Ser
65				70						75				80	

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Pro Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Glu Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Phe Val Gly Asp
1 5 10 15
Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Arg Asn Leu
20 25 30
Asn Trp Tyr Gln Gln Lys Pro Gly Thr Ala Pro Lys Val Leu Ile Tyr
35 40 45
Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro Glu
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Arg Thr
85 90 95
Phe Gly Gln Gly Thr Lys Val Glu Val Lys
100 105

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
1 5 10 15

Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Leu	Ser	Ser	Lys	Tyr
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Phe	Ile
		35					40					45			
Tyr	Asp	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Ser	Ile	Ser	Arg	Leu	Glu	Pro
	65				70					75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Gly	Thr	Pro	Arg	Thr
				85					90					95	
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105							

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGCTCACGC AGTCTCCAGG CACCCTGTCT TTGTCTCCAG GGGAAAGAGC CACCCTCTCC	60
TGCAGGGCCA GTCAGAGTGT TAGCAGCAAT TACTTAGCCT GGTACCAGCA GAGACCTGGC	120
CAGGCTCCCA GGCTCCTCAT CTATGGTGCA TCCAGCAGGG CCACTGGCAT CCCAGACAGG	180
TTCAGTGGCA GTGGGTCTGG GACAGACTTC ACTCTACCA TCAGCAGACT GGAGCCTGAA	240
GATTTTGCAG TGTATTACTG TCAGCTTTAT GGTAATCAC GTTGGACGTT CGGCCAAGGG	300
ACCAAGGTGG AGATCAAA	318

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGCTCACTC AGTCTCCAGC CACCCTGTCT TTGTCTCCAG GGGAAAGAGC CACCCTCTCC	60
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TGCAGGGCCA GTCAGAGTGT TAACAAGTAC TTAGCCTGGT ACCAACAGAA ACCTGGCCAG	120
GCTCCCAGGC TCCTCATCTA TGATGCATCC AACAGGGCCA CTGGCATCCC AGCCAGGTTC	180
AGTGGCAGTG GGTCTGGGAC AGACTTCACT CTCACCATCA GCAACCTAGA GCCTGAAGAT	240
TTTGCAGTTT ATTACTGTCA GCAGCGTAGC GACTGGGTCA CTTTCGGCGG AGGGACCAAG	300
GTGGAGATCA AA	312

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGCTCACGC AGTCTCCAGG CACCCTGTCT TTGTCTCCAG GGGAAAGAGC CACCCTCTCC	60
TGCGGGGCCA GTCAGAGTGT TAGGAGCAAC TACTTAGCCT GGTACCAGCA AAAACCTGGC	120
CAGGCTCCCA GGCTCCTCAT CTATGGTGTA TCCAGCAGGG CCACTGGCAT CCCAGACAGG	180
TTCAGTGGCA GTGGGTCTGG GACAGACTTC ACTCTACCA TCAGCAGACT GGAGCCTGAA	240
GATTTTGCAG TGTATTACTG TCAGCAGTAT GGTAGCTCAC CTCGGACTTT TGGCCAGGGG	300
ACCAAGTTGG AGATCAAA	318

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGCTCACGC AGTCTCCAGC CACCCTGTCT GTGTCTCCAG GGGAAAGAGC CTCCCTCTCC	60
TGCAGGGCCA GTCAGAGTGT CGGTAACAAT TTAGCTTGGT ATCAGCAGAA ACCTGGCCAG	120
GCTCCCAGGC TCCTCATTTA TGGTGGAAAC ACCAGAGCCA CTGGTACCCC AGACAGGTTC	180
AGTGGCAGTG GGTCTGGGAC AGAATTCAC CTCACCATCA GCAGCCTGCA GTCTGAGGAC	240

TTTGCAGTTT ATTTCTGTCA ACACTATAGT ACCTGGCCGC TCACTTTCGG CGGGGGGACC	300
AAGGTCGAGT TCAAG	315

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAGGTGCAGC TGCTCGAGTC TGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC	60
TCCTGTGCAG CGTCTGGATT CACCTTCAGT GCTTATGGCA TGCCTGGGT CCGCCAGGCT	120
CCAGGCAAGG GGCTGGAGTG GGTGGCAGGT ATATGGTTTG ATGGAAGTAA TCAATACTAT	180
TCAGACTCCG TGAAGGGCCG ATTCACCGTC TCCAGAGACA ATTCCAGGAA CACGCTGTTT	240
CTGCAAATGA ACAGCCTGAG ACCCGAGGAC ACGGCTGTCT ATTACTGTGC GACAGAGGTA	300
CTTTTTGGAT CGATTAAGGG GCGTTACTAC CTTGAAAAC TGGGGCCAGGG AACCTGGTC	360
ACCGTCTCCT CA	372

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGAGCTCA CCCAGTCTCC ATCGTCCCTG TCTGCATTTG TNGGAGACAG AGTCACCATC	60
ACTTGCCGGG CAAGTCAGAG TATTAGCAGG AACTTAAATT GGTATCAGCA GAAACCAGGG	120
ACAGCCCCTA AGGTCCTGAT CTATGCTGCA TCCAGTTTGC AAAGTGGGGT CCCATCGAGG	180
TTCAGTGGCA GTGGATCTGG GACAGATTTC ACTCTCACCA TCACCAGTCT GCAACCTGAA	240
GATTTTGCAA CTTACTATTG TCAACAGAGT TACACAACCC CTCGGACGTT CGGCCAAGGG	300
ACCAAGGTGG AAGTCAAA	318

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCCGAGCTCA CGCAGTCTCC AGGCACCCTG TCTTTGTCTC CAGGGGAAAG AGCCACCCTC	60
TCCTGCAGGG CCAGTCAGAG TCTTAGCAGC AAATACTTAG CNTGGTACCA ACAGAAACCT	120
GGCCAGGCTC CCAGGCTCTT CATTTATGAT GCATCCAGCA GGGCCACTGG CATCCCAGAC	180
AGGTTCACTG GCAGTGGGTC TGGGACAGAC TTCACTCTCA GCATCAGCAG ATTGGAGCCT	240
GAAGATTTTG CAGTGTATTA CTGTCAGCAG TATGGAACAC CTCGCACCTT CGGCCAGGGG	300
ACCAAGGTGG AAATCAAA	318

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCGAGCAGT CTGGGGCTGA GGTGAGGAAG CCTGGGTCTT CGGTGAAGGT CTCCTGCAAG	60
GCTTCTGGAG GCACCTTCAG CGGCCATGTT ATCACCTGGG TGCGACAGGC CCCTGGACAA	120
GGACTTGAGT GGATGGGAGA GAGCATCCCT ATCTTTGGTT CCGCAAATA CGCTCAAAAC	180
TACGCTCAGA AATTCCGGGA CAGAGTCTCG ATTATCGCGG ACGAATCCAC GAGCACGTCG	240
TTCATTGAGC TGAGCAACCT GAGATCTGAC GACACGGCCG TCTACTACTG TGCGAGAGAC	300
CCTCCAAGAT ATTGCAGTGC TGGTAGATGC TACCCGGGAT TCTTCCAGCA GTGGGGCCAG	360
GGCACCTCG TCACCGTCTC CTCA	384

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCGAGCAGT CTGGGGCTGA GGTGAAGAAG CCTGGGTCCT CGGTGAAGGT CTCCTGTCAG	60
TTTTTTGGAG ACACCTTCAG CAGATACACT ATTCAGTGGT TGCGACAGGC CCCTGGACAA	120
GGGCCTGAGT GGATGGGAAA TATCATCCCT GTCTATAATA CACCAAATA CGCGCAGAAG	180
TTTCAGGGCA GACTCTCGAT AACCGCCGAC GATTCCACGA GCACAGCCTA CATGGAAGTG	240
AGTAGCCTCA GATCTGAGGA CACGGCCGTC TATTTCTGTG CGAGAGTCGT AATACCAAAT	300
GCAATCCGGC ACACGATGGG ATATTACTTT GACTACTGGG GCCAGGGAAC CCTGGTCACC	360
GTCTCCTCA	369

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCGAGCAGT CTGGGGCTGA GGTGAAGAAG CCTGGGTCCT CAGTGAAGGT CTCCTGCAAG	60
GCTTCTGGAG GCACCTTCAG CGGCCATGTT ATCAGCTGGG TGCGACAGGC CCCTGGACAA	120
GGGCTTGAGT GGATGGGGGG GAGTATCTCT TTCTTTGGCA CATCAAATC CGCACAGAAG	180
TTCCAGGGCA GAGTCTCGAT TACCGCGGAC GAATCCGCGA GCACAGCCTA CATGGAGCTG	240
AGTAGCCTGA GATCGGAGGA CACGGCCATC TATTACTGTG CGAAAGACCC TCCAAGATT	300
TGTAGTGGTG GTAAGTGCTA CCCGGGGTTC TTCCAGCAGT GGGGCCAGGG CACCCTGGTC	360
ACCGTCTCCT CA	372

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCGAGTCGG GGGGAGGCGT GGTCCAGCCT GGGAGGTCCC TGAGACTCTC CTGTGCAGCG	60
TCTGGATTCA CCTTCAAGAC GTATGGCATG CACTGGGTCC GCCAGGCTCC AGGCAAGGGG	120
CTGGAGTGGG TGGCAGGTAT TTCGTTTGAT GGAAGTAACC AATATTACGC AGACTCCGTG	180
AAGGGCCGAT TCATCGTCTC CAGAGACAAT TCCAGGGACA CGGTGTTTCT GCAGATGAGC	240
AGCCTGAGAC TCGAGGACAC GGCTGTCTAT TACTGTGCGA CAGAGGGTTC TCCTTTTGGC	300
TCGATTAAGG GGC GTTACTA CCTTGAAAAT TGGGGCCAGG GAACCCTGGT CACCGTCTCC	360
TCA	363

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGGTGCAGC TGCTCGAGTC GGGCCCAGGA CTGGTGAAGC CTTCGGGGAC CCTGTCCCTC	60
ACCTGCACTG TCTCTGGTGG CTCCATCAGG AGCAGTCACT GGTGGAGTTG GGTCCGCCAG	120
CCCCCAGGGA AGGGACTGGA GTGGATTGGA GAAGTCTTTT TTAGTGGAAG CACCATCTAC	180
AACCCATCCC TCAACGATCG AGTCTTCATG TCTGTAGACA AGTCCAAGGA CCAGGTCTCC	240
CTGAGGCTGA GCTCTGTGAC CGCCGCGGAC ACGGCCGTGT ATTACTGTGC GAGATCCCCC	300
ATAAAAATGA ATCAGGGAAG AATGATGTTG GATGCCTTTG ATATCTGGGG CCAGGGGACA	360
CTCGTCATCG TCTCTTCC	378

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 378 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAGGTGCAGC TGCTCGAGTC TGGGTCTGAG GTGAAGAAGC CTGGGTCTTC GGTGAAGGTC	60
TCCTGCAGGG CCTCTGGAGG CAGCTTCAGA AGCTACAATT TCAATTGGGT GCGACAGGCC	120
CCTGGACAAG GTCTTGAGTG GATGGGAGGC ATCATCCCTA TGTTGGAAC AGCAAACCTAC	180
GCACAGAAGT TTCAGGGCAG AGTCACAATT ACCGCGGACG AATCCACGGC CACAGGCTAC	240
ATGGAGTTGA GCAGTCTGAG ATCTGAAGAC ACGGCCGTTT ATTACTGTGC GATGCCCTAT	300
CCAAAACATT GCAGTCGTGG AAGTTGCTGG GGCTGGTTCG ACCCCTGGGG CCAGGGAAC	360
CTGGTCACCG TGTCTTCA	378

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val	Ala	Gly	Val	Asp	Ala	Ser	Thr	Tyr	Thr	Thr	Gly	Gly	Gln	Ser	Gly
1			5					10					15		
Arg	Thr	Thr	Tyr	Gly	Ile	Val	Gly	Leu	Phe	Ser	Leu	Gly	Pro	Ser	Gln
			20				25					30			
Lys	Leu	Ser	Leu	Ile	Asn	Thr	Asn	Gly	Ser	Trp	His	Ile	Asn	Arg	
		35				40					45				

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAACGCAATT AATGTGAGTT AG	22
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(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCCCCTTAT TAGCGTTTGC CATC

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAGAAGTTG TTCAGCAGGC A

21

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAGACAGCTA TCGCGATTGC AG

22

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTCGTTGACC AGGCAGCCCA G

21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACCTATTGCC TACGGCAGCC G

21